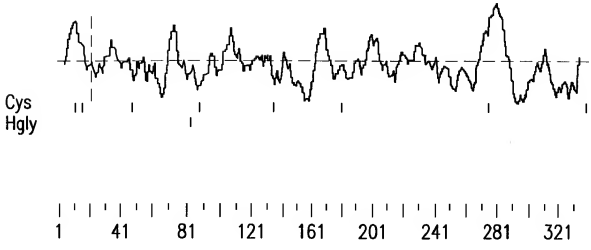
```
                                                M  S  P  S  P  T  A  L  F  C  L   11
GGAGTCGACCCACGCGTCCGCAGGGCTGAGGAACC ATG TCT CCA TCC CCG ACC GCC CTC TTC TGT CTT   68

 G  L  C  L  G  R  V  P  A  Q  S  G  P  L  P  K  P  S  L  Q                     31
GGG CTG TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG  128

 A  L  P  S  S  L  V  P  L  E  K  P  V  T  L  R  C  Q  G  P                     51
GCT CTG CCC AGC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT  188

 P  G  V  D  L  Y  R  L  E  K  L  S  S  S  R  Y  Q  D  Q  A                     71
CCG GGC GTG GAC CTG TAC CGC CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA  248

 V  L  F  I  P  A  M  K  R  S  L  A  G  R  Y  R  C  S  Y  Q                     91
GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CGC TAC CGC TGC TCC TAC CAG  308

 N  G  S  L  W  S  L  P  S  D  Q  L  E  L  V  A  T  G  V  F                    111
AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT  368

 A  K  P  S  L  S  A  Q  P  G  P  A  V  S  S  G  G  D  V  T                    131
GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC  428

 L  Q  C  Q  T  R  Y  G  F  D  Q  F  A  L  Y  K  E  G  D  P                    151
CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT  488

 A  P  Y  K  N  P  E  R  W  Y  R  A  S  F  P  I  I  T  V  T                    171
GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CGG GCT AGT TTC CCC ATC ATC ACG GTG ACC  548

 A  A  H  S  G  T  Y  R  C  Y  S  F  S  S  R  D  P  Y  L  W                    191
GCC GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG  608

 S  A  P  S  D  P  L  E  L  V  V  T  G  T  S  V  T  P  S  R                    211
TCG GCC CCC AGC GAC CCC CTG GAG CTT GTG GTC ACA GGA ACC TCT GTG ACC CCC AGC CGG  668

 L  P  T  E  P  P  S  S  V  A  E  F  S  E  A  T  A  E  L  T                    231
TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC  728

 V  S  F  T  N  K  V  F  T  T  E  T  S  R  S  I  T  T  S  P                    251
GTC TCA TTC ACA AAC AAA GTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA  788

 K  E  S  D  S  P  A  G  P  A  R  Q  Y  Y  T  K  G  N  L  V                    271
AAG GAG TCA GAC TCT CCA GCT GGT CCT GCC CGC CAG TAC TAC ACC AAG GGC AAC CTG GTC  848

 R  I  C  L  G  A  V  I  L  I  I  L  A  G  F  L  A  E  D  W                    291
CGG ATA TGC CTC GGG GCT GTG ATC CTA ATA ATC CTG GCG GGG TTT CTG GCA GAG GAC TGG  908

 H  S  R  R  K  R  L  R  H  R  G  R  A  V  Q  R  P  L  P  P                    311
CAC AGC CGG AGG AAG CGC CTG CGG CAC AGG GGC AGG GCT GTG CAG AGG CCG CTT CCG CCC  968
```

FIG.1A

```
 L  P  P  L  P  Q  T  R  K  S  H  G  G  Q  D  G  G  R  Q  D  331
CTG CCG CCC CTC CCG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT 1028

 V  H  S  R  G  L  C  S  *                                   340
GTT CAC AGC CGC GGG TTA TGT TCA TGA                         1055

CCGCTGAACCCCAGGCACGGTCGTATCCAAGGGAGGGATCATGGCATGGGAGGCGACTCAAAGACTGGCGTGTGTGGAG 1134

CGTGGAAGCAGGAGGGCAGAGGCTACAGCTGTGGAAACGAGGCCATGCTGCCTCCTCCTGGTGTTCCATCAGGGAGCCG 1213

TTCGGCCAGTGTCTGTCTGTCTGCCTCTCTGTCTGAGGGCACCCTCCATTTGGGATGGAAGGAATCTGTGGAGAC 1292

CCCATCCTCCTCCCTGCACACTGTGGATGACATGGTACCCTGGCTGGACCACATACTGGCCTCTTTCTTCAACCTCTCT 1371

AATATGGGCTCCAGACGGATCTCTAAGGTTCCCAGCTCTCAGGGTTGACTCTGTTCCATCCTCTGTGCAAAATCCTCCT 1450

GTGCTTCCCTTTGGCCCTCTGTGCTCTTGTCTGGTTTTCCCCAGAAACTCTCACCCTCACTCCATCTCCCACTGCGGTC 1529

TAACAAATCTCCTTTCGTCTCTCAGAACGGGTCTTGCAGGCAGTTTGGGTATGTCATTCATTTTCCTTAGTGTAAAACT 1608

AGCACGTTGCCCGCTTCCCTTCACATTAGAAAACAAGATCAGCCTGTGCAACATGGTGAAACCTCATCTCTACCAACAA 1687

AACAAAAAAACACAAAAATTAGCCAGGTGTGGTGGTGCATCCCTATACTCCCAGCAACTCGGGGGGCTGAGGTGGGAGA 1766

ATGGCTTGAGCCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCTAGCTCGGGTGACGAAGCCTGA 1845

CCTTGTCTCAAAAAATACAGGGATGAATATGTCAATTACCCTGATTTGATCATAGCACGTTGTATACATGTACTGCAAT 1924

ATTGCTGTCCACCCCATAAATATGTACAATTATGTATACATTTTTAAAATCATAAAAATAAGATAATGAAAAAAAAAAA 2003

AAAAAAAAAAAAAAGGGCGGGCCGCTAGACTAGTCTAGAGAACA                2047
```

FIG.1B



MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLE
KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP
GPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRC
YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT
TETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVILIILAGFLAEDWHSRRKRLRH
RGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIG.2

```
                10        20        30        40        50        60        70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       :::.: ::  :::   :: ::::: :::: :::::::::.:::::: :  .: .:: ::  ::::. .:
       ATGTCTCCATCCCCGACCGCCCTCTTCTGTCTTGGGCTGTGTCTGGGGCG-TGTGCCAGC--GCAGAGTG
                10        20        30        40        50        60

                80        90       100       110       120       130
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGAT-CAGCTGGGGGAGCCCCGTGACCA
       :.::  ::::::::.:::::::: .:::: .::: .:::: ::.: :  ::::.:.::::  ::::::
       GACCGCTCCCCAAGCCCTCCCTCCAGGCTCTGCCCAGCTCCCTGGTGCCCCTGGAGAAGCCA-GTGACCC
        70        80        90       100       110       120       130

     140       150       160       170       180       190       200
inputs TCTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGA
       :: :::: ::::: .:::      ::.:: ::.  ::: :..          ::: .:::      ...
       TCCGGTGCCAGGG--ACCT------CCGGGCGTG--GACCTGTA--------CCGCCTGGAG-----AAG
         140       150       160       170       180

     210       220       230       240       250       260       270
inputs CAGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCG
       :.::..:  :: .:.::.::: :.::.:: ::: .   ::: ::::::. :::::: .... . :. :: 
       CTGAGTT--CCAGCAGGTACC-AGGATCA-GGCAGTCCTCTTCATCCCGGCCATGAAGAGAAGTCTGGCT
          190       200       210       220       230       240

     280       290       300       310       320       330       340
inputs GGGAGATACCGCTGCCACTATTACAGCTCTGCAG--GCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGT
       :: : :::::::::  :::   ::: .: : ::   ::::::  .:::::::::::  :::::::: ::
       GGACGCTACCGCTGCTCCTAC--CAGAACGGAAGCCTCTGGTCCCTGCCCAGCGACCAGCTGGAGCTCGT
     250       260       270       280       290       300       310

       350       360       370       380       390       400       410
inputs GATGACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAAT
        .  ::.::: : :. . :::::::.: ::::::::::.::::.:::: : :::: : :::::.:::.:
       TGCCACGGGAGTTTTTGCCAAACCCTCGCTCTCAGCCCAGCCCGGCCCGGCGGTGTCGTCAGGAGGGGAC
       320       330       340       350       360       370       380

       420       430       440       450       460       470       480
inputs ATGACCCTCCGATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGC
       .:.::::: :..::: . .:.:.:.: :: :.: ::::.:::: :::::. ::::::::
       GTAACCCTACAGTGTCAGACTCGGTATGGCTTTGACCAATTTGCTCTGTACAAGGAAGG----------
       390       400       410       420       430       440

       490       500       510       520       530       540       550
inputs TCCCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGT
             ::::::::                                :   :::::.              :..
       ------GGACCCTG--------------------------------C---GCCCTA-------------CAA
             450                                         460
```

FIG.3A

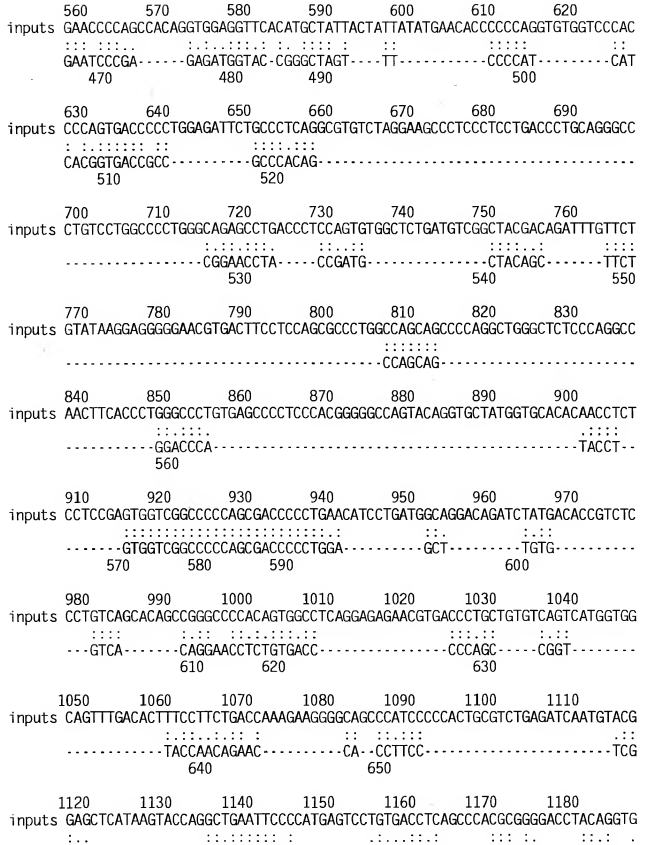


FIG.3B

Docket No.: 7853-234-999
Serial No.: 09/829,495
Inventor(s): BUSFIELD ET AL.
Title: "GLYCOPROTEIN VI AND USES THEREOF"

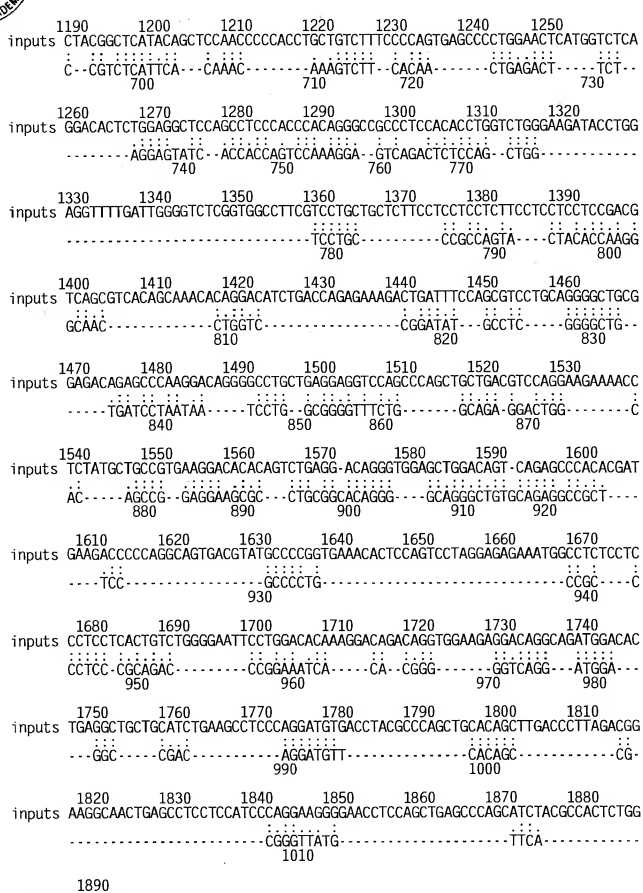


FIG.3C

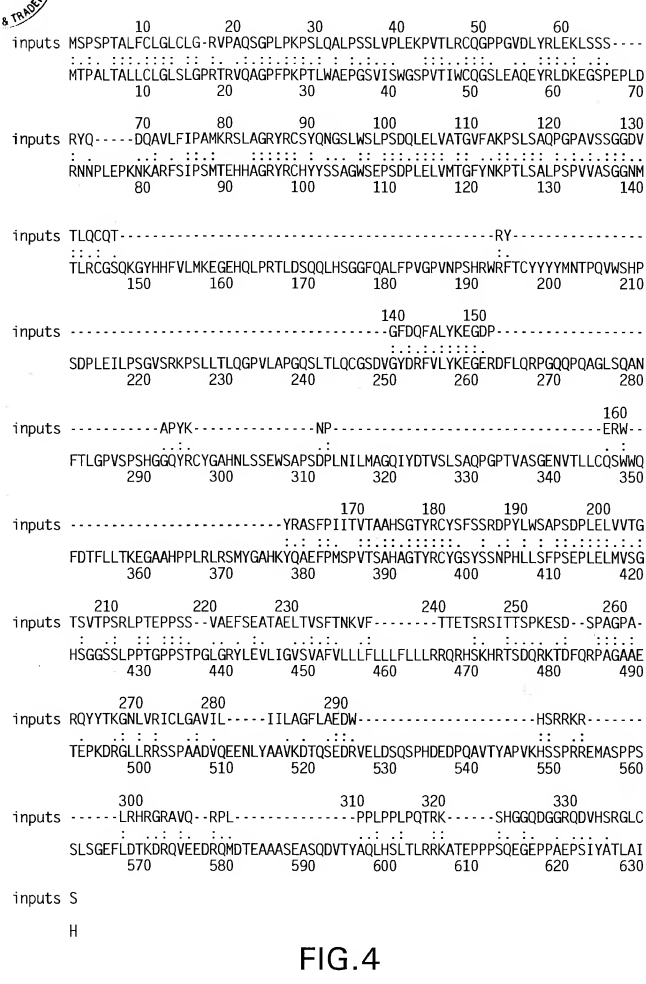


FIG.4

```
            *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
               + vtL+C+         + v  y +  k  ++         r++ +
hT268    41    EKPVTLRCQGP------PGVDLY-RLEKlSSS--------RYQDQ-- 70

               anlsegrfsissltLtissvekeDsGtYtCvv<-*
                           ++L i   +++ +G Y+C
hT268    71    -----------AVLFIPAMKRSLAGRYRCSY    90
```

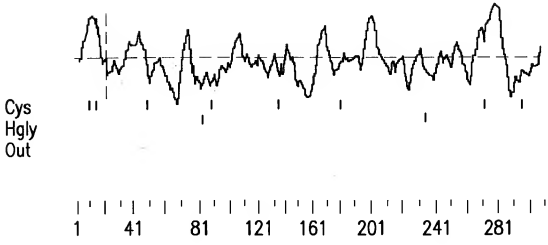
FIG.5A

```
            *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
               G++vtL+C+++     +  ++  y k+g++ +      y+++
hT268   127    GGDVTLQCQTR---YGFDQFALY-KEGDpAP-----YKNPERWYR-- 162

               anlsegrfsissltLtissvekeDsGtYtCvv<-*
                           ++++i++v++  sGtY+C
hT268   163    -----------ASFPIITVTAAHSGTYRCYS    182
```

FIG.5B

```
                                                                  M   S   P   A     4
GAGTCGACCCACGCGTCCGCTTCCCTGCTTGGCCACATAGCTCAGGACTGGGTTGCAGAACC ATG TCT CCA GCC    74

 S   P   T   F   F   C   I   G   L   C   V   L   Q   V   I   Q   T   Q   S   G    24
TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GTG ATC CAA ACA CAG AGT GGC   134

 P   L   P   K   P   S   L   Q   A   Q   P   S   S   L   V   P   L   G   Q   S    44
CCA CTC CCC AAG CCT TCC CTC CAG GCT CAG CCC AGT TCC CTG GTA CCC CTG GGT CAG TCA   194

 V   I   L   R   C   Q   G   P   P   D   V   D   L   Y   R   L   E   K   L   K    64
GTT ATT CTG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA   254

 P   E   K   Y   E   D   Q   D   F   L   F   I   P   T   M   E   R   S   N   A    84
CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT   314

 G   R   Y   R   C   S   Y   Q   N   G   S   H   W   S   L   P   S   D   Q   L   104
GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT   374

 E   L   I   A   T   G   V   Y   A   K   P   S   L   S   A   H   P   S   S   A   124
GAG CTA ATT GCT ACA GGT GTG TAT GCT AAA CCC TCA CTC TCA GCT CAT CCC AGC TCA GCA   434

 V   P   Q   G   R   D   V   T   L   K   C   Q   S   P   Y   S   F   D   E   F   144
GTC CCT CAA GGC AGG GAT GTG ACT CTG AAG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC   494

 V   L   Y   K   E   G   D   T   G   P   Y   K   R   P   E   K   W   Y   R   A   164
GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC   554

 N   F   P   I   I   T   V   T   A   A   H   S   G   T   Y   R   C   Y   S   F   184
AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC   614

 S   S   S   S   P   Y   L   W   S   A   P   S   D   P   L   V   L   V   V   T   204
TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GTG GTT ACT   674

 G   L   S   A   T   P   S   Q   V   P   T   E   E   S   F   P   V   T   E   S   224
GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAA GAA TCA TTT CCT GTG ACA GAA TCC   734

 S   R   R   P   S   I   L   P   T   N   K   I   S   T   T   E   K   P   M   N   244
TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT   794

 I   T   A   S   P   E   G   L   S   P   P   I   G   F   A   H   Q   H   Y   A   264
ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC   854

 K   G   N   L   V   R   I   C   L   G   A   T   I   I   I   I   L   L   G   L   284
AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT   914

 L   A   E   D   W   H   S   R   K   K   C   L   Q   H   R   M   R   A   L   Q   304
CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA   974

 R   P   L   P   P   L   P   L   A   *                                           314
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG                                        1004

AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCACAACCATGGACATCACCACTAGAGCCACAGACAT 1083
GGACATACTCAAGAGTGGGGAGGTTATATAAAAAATGAGTGTGGAGAATAAATGCAGAGCCAACAAGGTGAAAAAAAA 1162
A                                                                              1163
```

FIG.6



MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYR
CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTEESFPVTESSRRPSILPTNKISTTE
KPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIG.7

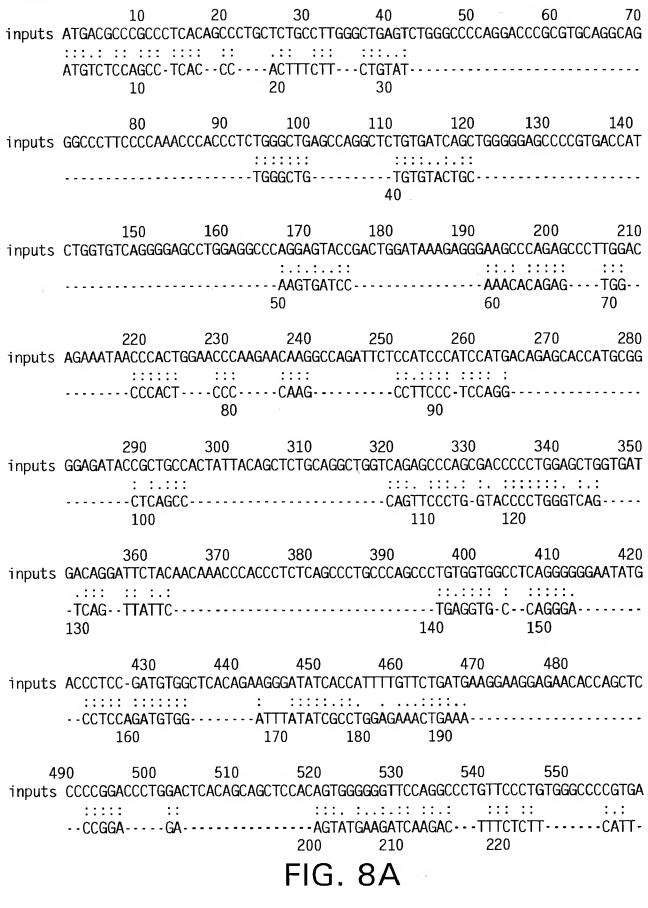


FIG. 8A

```
          560        570        580        590        600        610        620
inputs ACCCCAGCCACAGGTGGAGGTTCACATGCTATTACTATTATATGAACACCCCCCAGGTGTGGTCCCACCC
          :::.::: .:...::.::.  :::::                :.::          ::::.:
       ---CCAACCATGGAAAGAAGTA---ATGCT-------------GGAC--------GGTAT----------
        230        240        250                              260

          630        640        650        660        670        680        690
inputs CAGTGACCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCCCT
       :..::   : :: .            ::::.      ..::.:: :                .:.:: : ::
       CGATG---CTCTTA----------TCAGA------ATGGGAGTC---------------ACTGGTCTCT
                270                        280                        290

          700        710        720        730        740        750        760
inputs GTCCTGGCCCCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCTGT
                :::..:         :::::  : .:.:     ::.::    :::::
       --------CCCAAG--------TGACCAGCTTGAG-----CTAATT---GCTAC----------------
          300              310            320

          770        780        790        800        810        820        830
inputs ATAAGGAGGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCCAGGCCAA
          :::.: : ...: .::  ::::                                    .:::::
       ---AGGTGTGTATGCTAAAC--CCTC----------------------------ACTCTC---------
          330        340                                    350

          840        850        860        870        880        890        900
inputs CTTCACCCTGGGCCCTGTGAGCCCCTCCCACGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCTCC
                          ::: : :::::                 :::
       ------------------AGCTCATCCCA----------------GCT--------------------
                         360

          910        920        930        940        950        960        970
inputs TCCGAGTGGTCGGCCCCCAGCGACCCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGTCTCCC
                        :::::. :::        ::   :.:::::::   :::  .::::.: :.
       ----------------CAGCAGTCCC-------TC---AAGGCAGG---GAT--GTGACTCTGA-----
                       370                380          390          400

          980        990        1000       1010       1020       1030       1040
inputs TGTCAGCACAGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTGTGTCAGTCATGGTGGCA
       .::        :::.:. :::: :                                        :::: .::.::.
       AGT-------GCCAGAGCCCATA-------------------------------------CAGTTTTGATGA--
                       410                                          420

         1050       1060       1070       1080       1090       1100       1110
inputs GTTTGACACTTTCCTTCTGACCAAAGAAGGGGCAGCCCATCCCCCACTGCGTCTGAGATCAATGTACGGA
               .::: ::::.. ::::::::::::     ::     :::: : :: : :  :...:  : ::
       --------ATTCGTTCTATACAAAGAAGGGG------AT-----ACTGGGCCTTATA--AGAGACCTGA
               430        440        450                460        470
```

FIG.8B

Docket No.: 7853-234-999
Serial No.: 09/829,495
Inventor(s): BUSFIELD ET AL.
Title: "GLYCOPROTEIN VI AND USES THEREOF"

```
          1120       1130       1140       1150       1160       1170       1180
inputs GCTCATAAGTACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCGGGGACCTACAGGTGCT
       :   :...:::::.::: .:.:::::::: :   :.:::::  :.:: :::.  ::::: ::: :::: :
       G--AAATGGTACCGGGCCAATTTCCCCATCATCACAGTGACTGCTGCTCACAGTGGGACGTACCGGTGTT
          480        490        500        510        520        530        540

          1190       1200       1210       1220       1230       1240       1250
inputs ACGGCTCATACAGCTCCAACCCCCACCTGCTGTCTTTCCCCAGTGAGCCCCTGGAACTCATGGTCTCAGG
       ::.::: : :::::: . ::  :::::  :::. ::: ::::: :: ::.:.::  .:::: .:.::
       ACAGCTTCTCCAGCTCATCTCCATACCTGTGGTCAGCCCCGAGTGACCCTCTAGTGCTTGTGGTTACTGG
          550        560        570        580        590        600        610

          1260       1270       1280       1290       1300       1310       1320
inputs ACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCTGGTCTGGGAAGATACCTGGAG
       ::.::::::      :::  :::::: ::  :::   .::::.       ::. .:... ..:.:::
       ACTCTCTG------CCA--CTCCCAGCC--AGGT--ACCCAC-------GGA-AGAATCATTTCCTG---
          620              630              640              650        660

          1330       1340       1350       1360       1370       1380       1390
inputs GTTTTGATTGGGGTCTCGGTGGCCTTCGTCCTGCTGCTCTTCCTCCTCCTCTTCCTCCTCCGACGTC
          :::          :.:.. :::    ::.: .:  :::::.     :::: :    ::.: .:::.
       ----TGA---------CAGAATCCT----CCAGGAGACCTTCCA-----TCTTAC----CCACAAACAAA
                  670              680              690              700

          1400       1410       1420       1430       1440       1450       1460
inputs AGCGTCACAGCAAACACAGGACATCTGACCAGAGAAAGACTGATTTCCAGCGTCCTGCAGGGGCTGCGGA
       :   : .:..:::   :.:.:    ...:::..:::...:  : : :: : :::.: ::::::::
       A---TATCTACAA---CTGAA----AAGCCTATGAATATC--ACTGCCT-C-TCCAG-AGGGGCTG----
     710          720          730          740          750

          1470       1480       1490       1500       1510       1520       1530
inputs GACAGAGCCCAAGGACAGGGGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACCTC
          :::::.          ::    :. .:::  .:: :: :.::.          :
       -----AGCCCT----------CC-----AATTGGTTTTGCTCATCAGCA------------------C
             760                      770        780

          1540       1550       1560       1570       1580       1590       1600
inputs TATGCTGCCGTGAAGGACACACAGTCTGAGGACAGGGTGGAGCTGGACAGTCAGAGCCCACACGATGAAG
       :::::                          ::.:: :.: ::::.:              ::.. :.:
       TATGC--------------------------CAAGGGGAATCTGGTC-------------CGGATATG
        790                             800                         810

          1610       1620       1630       1640       1650       1660       1670
inputs ACCCCCAGGCAGTGACGTATGCCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCCTCTCCTCCCTC
          :: .::          :::: ::.:                 :: .: :....::
       ---CCTTGG----------TGCCACGAT--------------TATAATAATTTTGT------------
             820              830                    840

          1680       1690       1700       1710       1720       1730       1740
inputs CTCACTGTCTGGGGAATTCCTGGACACAAAGGACAGACAGGTGGAAGAGGACAGGCAGATGGACACTGAG
             ::::: .:  ::.:   ::.::: .:.:            :::: :.:.:.:.     :
       ---------TGGGGCTT--CTAG---CAGAGGATTGGC-----------ACAGTCGGAAGAA-----AT
                850              860                    870        880
```

FIG.8C

```
   1750       1760       1770       1780       1790       1800       1810
inputs GCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGGAAGG
       ::  :::::.:.          ::::::::.::                :::: .:          .::::
       GC--CTGCAACA---------CAGGATGAGA-----------------GCTTTGC---------AAAGG
             890                900                          910

   1820       1830       1840       1850       1860       1870       1880
inputs CAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGGCCAT
       : :::.     ::.::               :::::                          :.:::::::
       CCACTA-----CCACC---------------CCTCC----------------------CACTGGCC--
         920                          930

   1890
inputs CCAC
```

FIG. 8D

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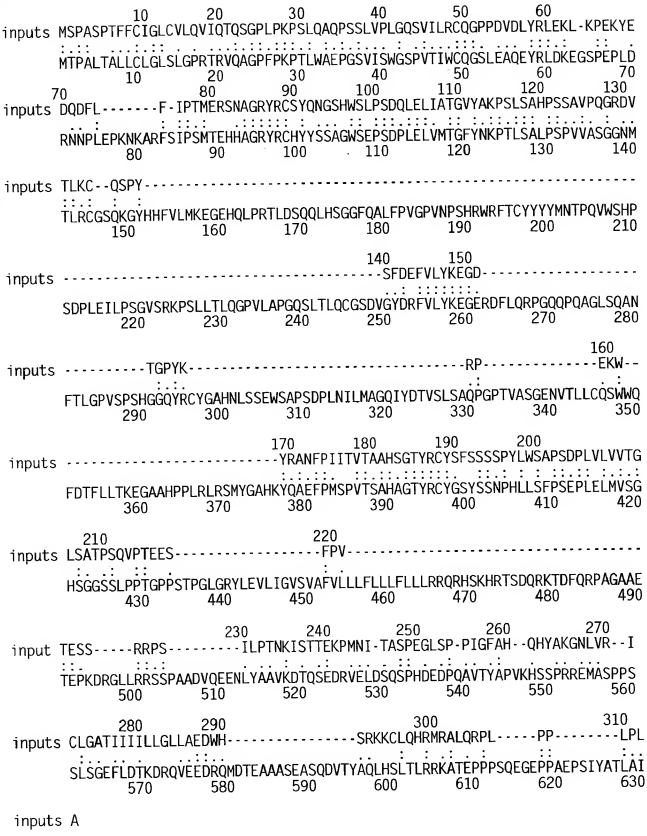

FIG. 9

```
            *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
               G+sv L+C+         ++v  y +  k ++         +++e +
mT268    42    GQSVILRCQGP------PDVDLY-RLEKIKP--------EKYEDQ-- 71

               anlsegrfsissltLtissvekeDsGtYtCvv<-*
                           L i + e++++G Y+C
mT268    72    -----------DFLFIPTMERSNAGRYRCSY    91
```

FIG.10A

```
            *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
               G +vtL C++         ++  y k+g++ +       Y+r+e   +
mT268    128   GRDVTLKCQSP---YSFDEFVLY-KEGDtGP-------YKRPEKW-Y 162

               anlsegrfsissltLtissvekeDsGtYtCvv<-*
               +             ++j++v++  sGtY+C
mT268    163   RA----------NFPIITVTAAHSGTYRCYS    183
```

FIG.10B

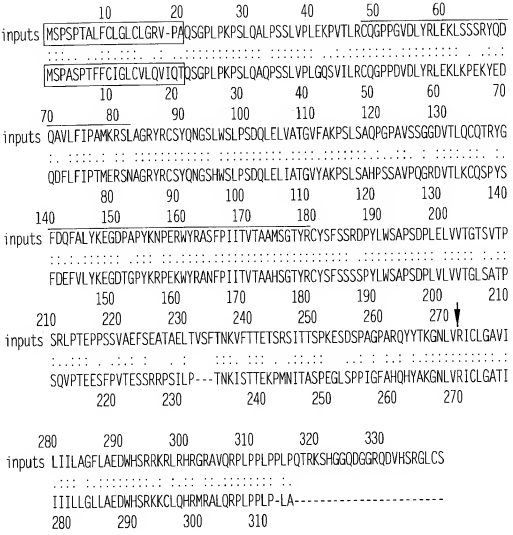

FIG.11

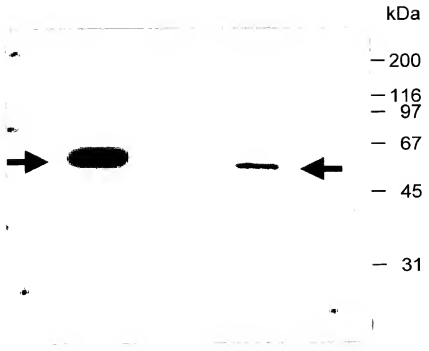

FIG.12

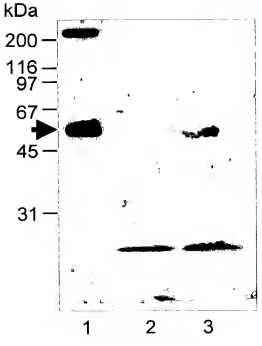

FIG.13A

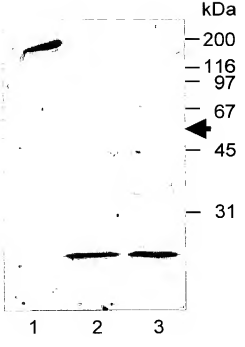

FIG.13B

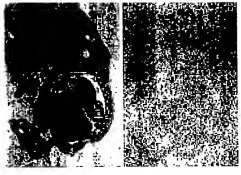

FIG.14A

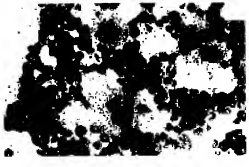

FIG.14B

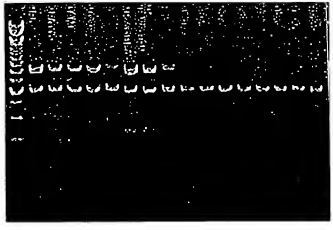

FIG.14C

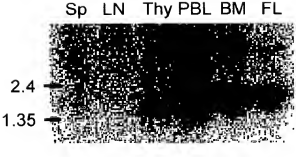

FIG.14D

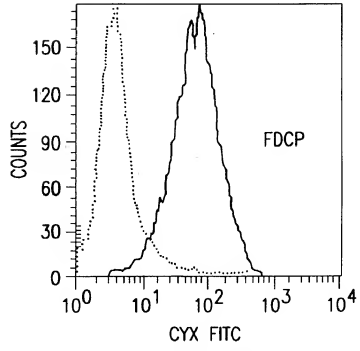

FIG.15A

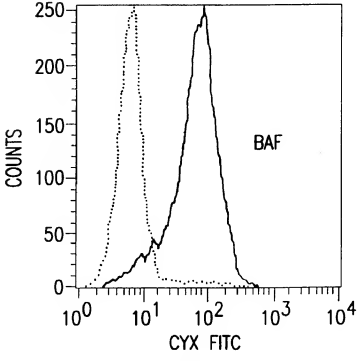

FIG.15B

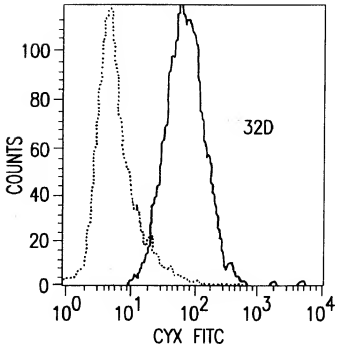

FIG.15C

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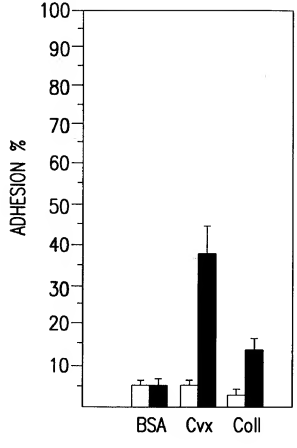

FIG.16A

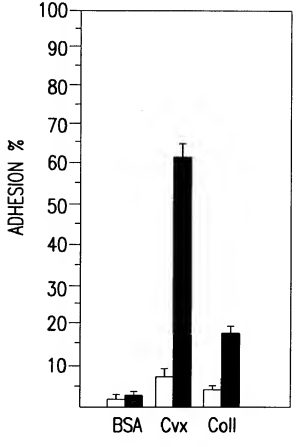

FIG.16B

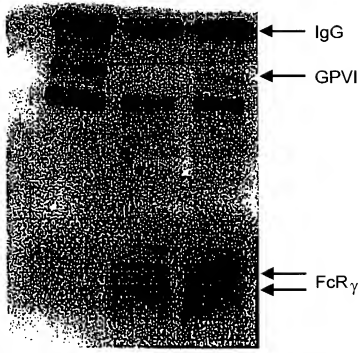

FIG.17

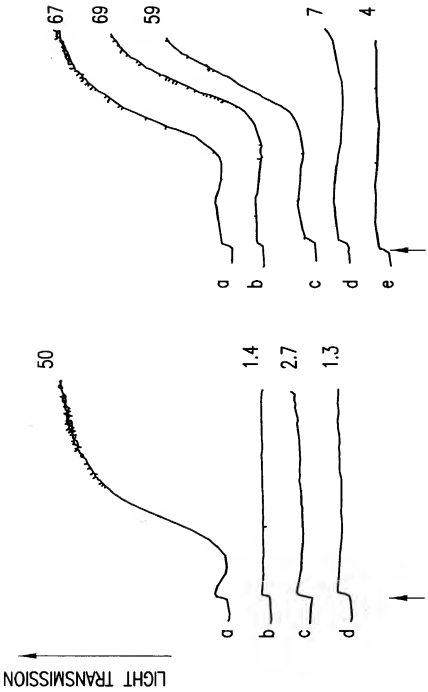

FIG.18A

FIG.18B

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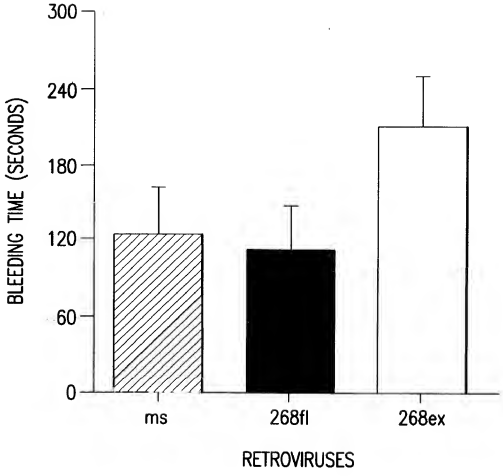


FIG.19

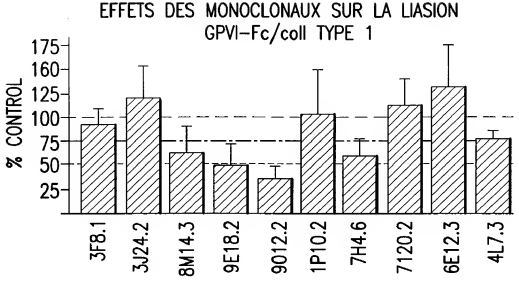


FIG.20

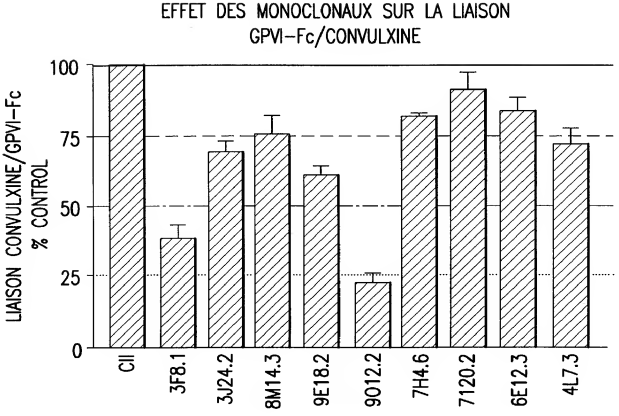


FIG.21

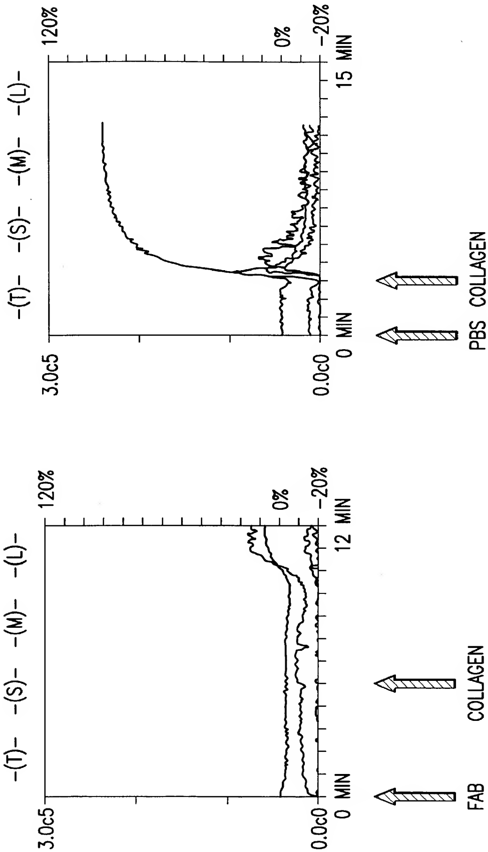


FIG.22

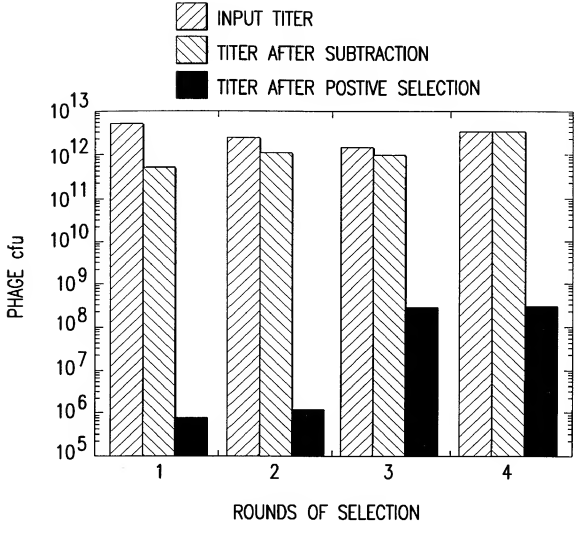


FIG.23

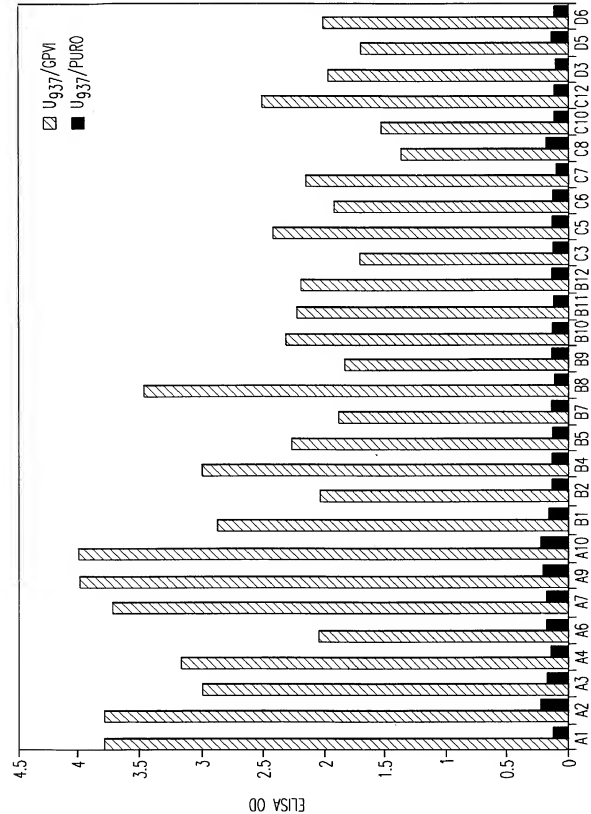


FIG.24A

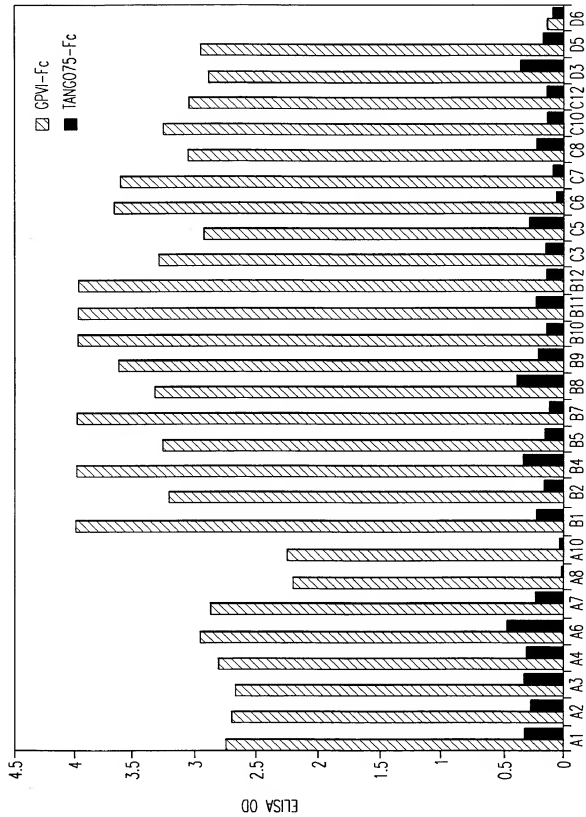


FIG.24B

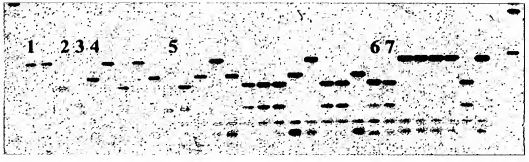


FIG.25

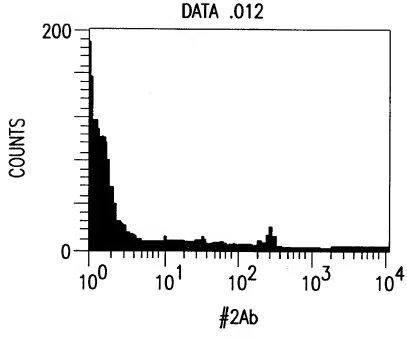


FIG.26A

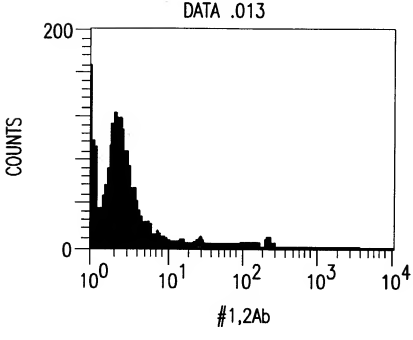


FIG.26B

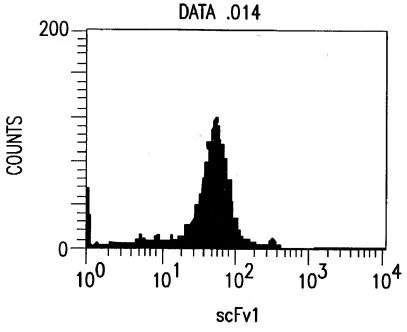


FIG.26C

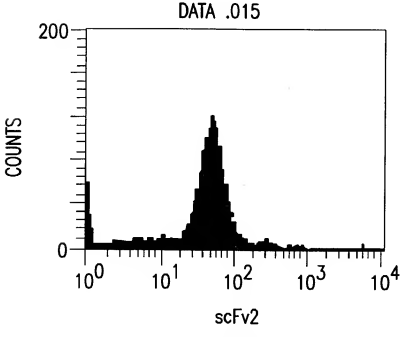


FIG.26D

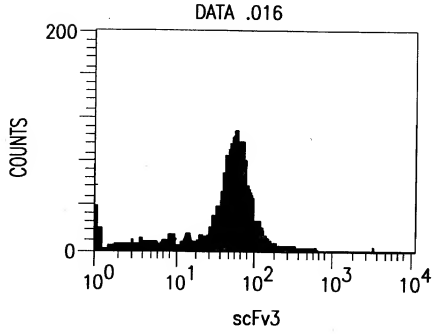


FIG.26E

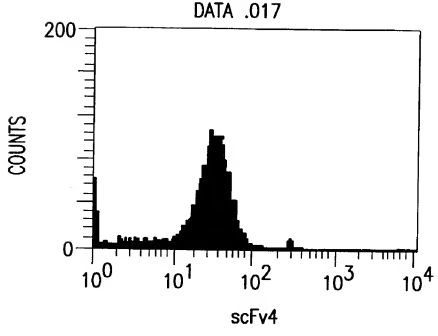


FIG.26F

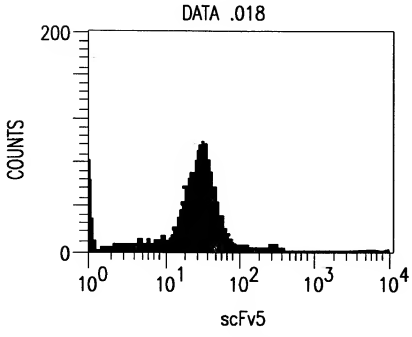


FIG.26G

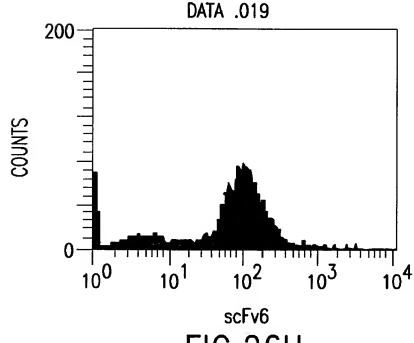
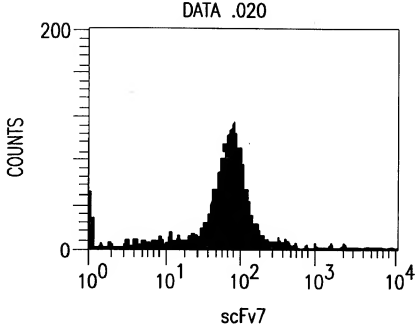


FIG.26H



scFv1:A4
scFv2:B4
scFv3:A9
scFv4:C4
scFv5:C9
scFv6:C10
scFv7:A10

FIG.26I

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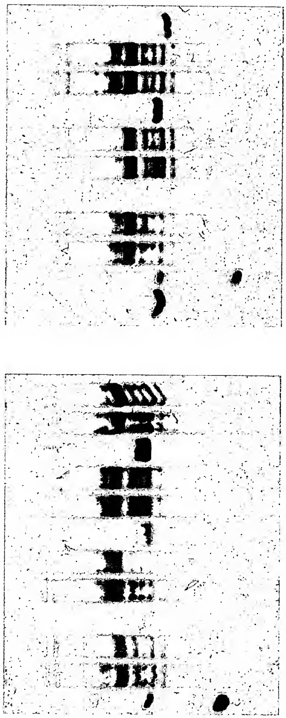
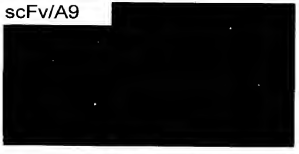


FIG.27

control scFv

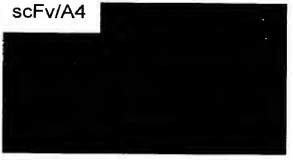
scFv/A9



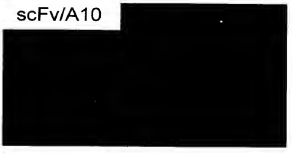
scFv/C3

FIG.28A

scFv/A4



scFv/A10



scFv/C9

FIG.28B

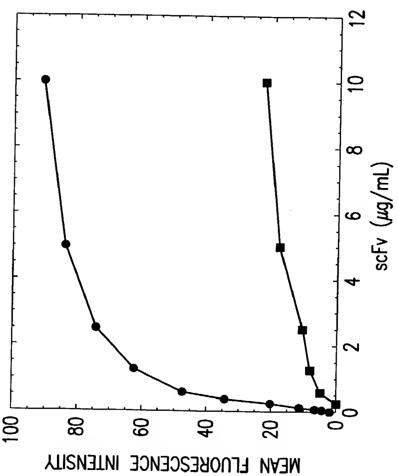


FIG.29A

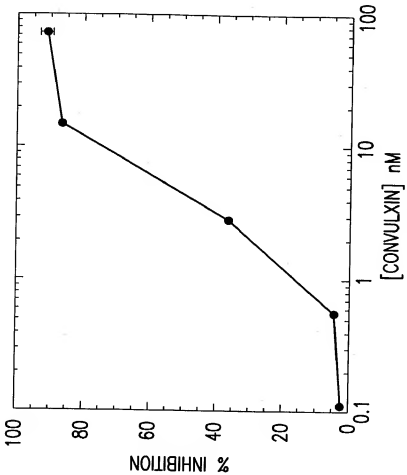


FIG.29B

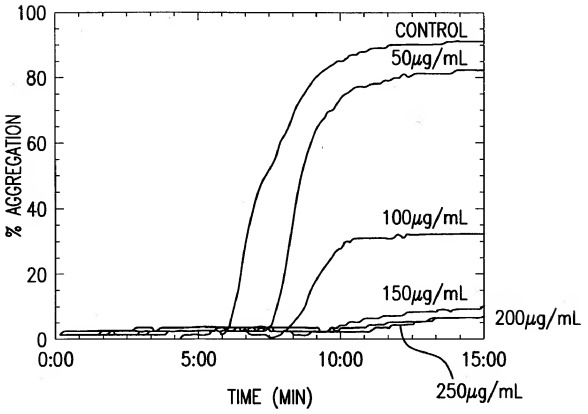


FIG.30A

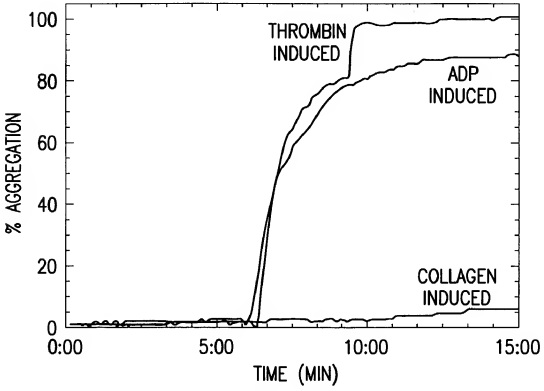


FIG.30B